

Supporting Information for

Effects of composting different types of organic fertilizer on the microbial community structure and antibiotic resistance genes

Figures:

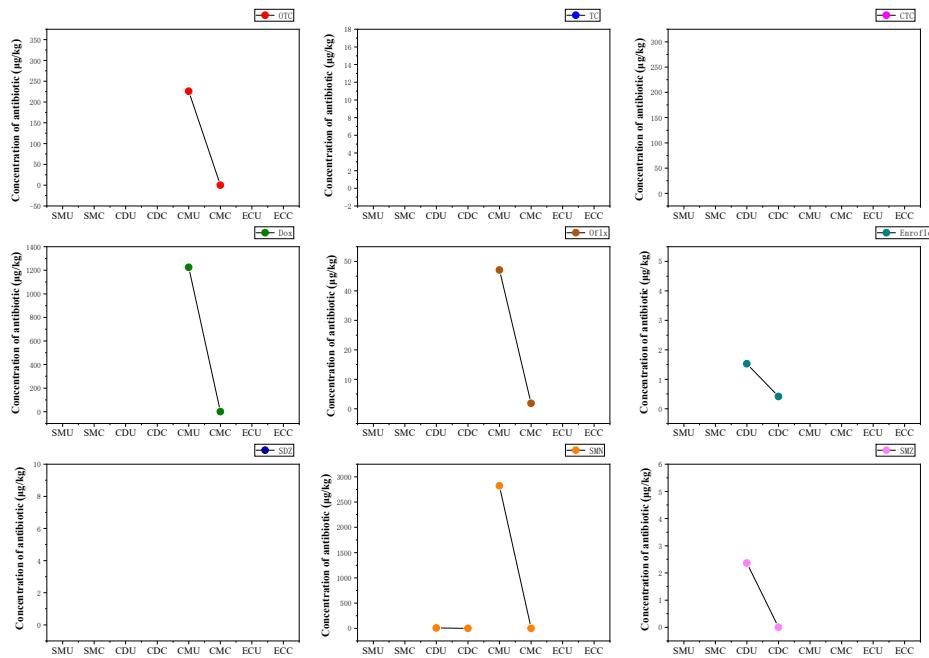


Figure S1. Changes in antibiotic residues before and after composting; unmarked items were not measured. (sulfadiazine (SDZ), oxytocin (OTC), sulfamethazine (SMZ), chlortetracycline (CTC), sulfamethoxypyridazine (SMN), TC, ofloxacin (Oflox), doxycycline (Dox) and enrofloxacin (Enroflox)).

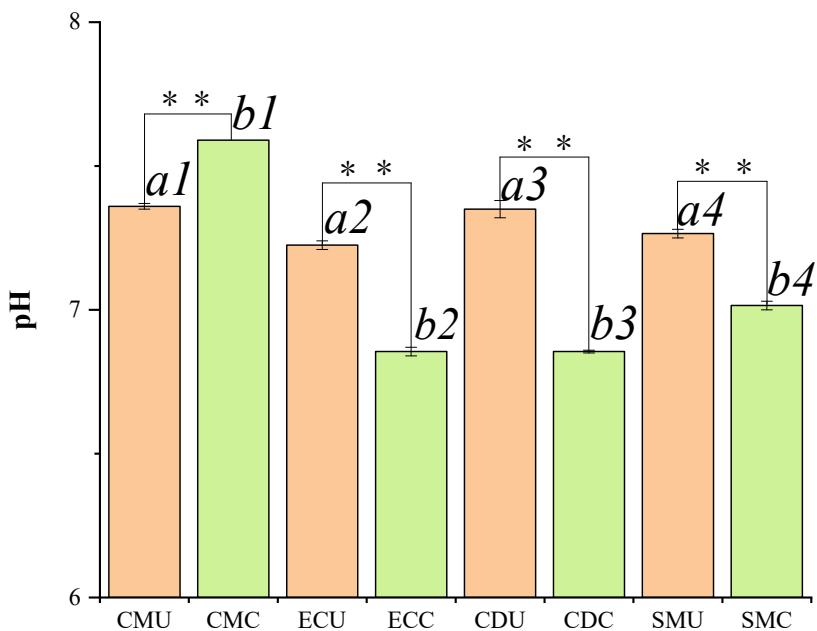


Figure S2. Change in pH before and after composting of organic fertilizers. Each value was a mean of three replicates. The same letter + different numbers within a group indicate significant differences at $p < 0.001$ (ANOVA test; $n = 3$). ** ($p < 0.01$) on the bar indicates a statistically significant difference.

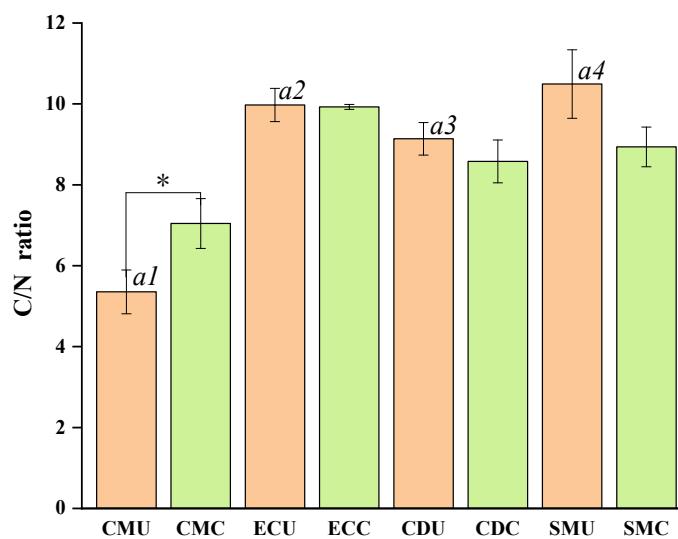


Figure S3. Differences in the C/N ratio before and after composting of five organic

fertilizers. The same letter + different numbers within a group indicate significant differences at $p < 0.001$ (ANOVA test; $n = 3$). * ($p < 0.05$) on the bar indicates a statistically significant difference.

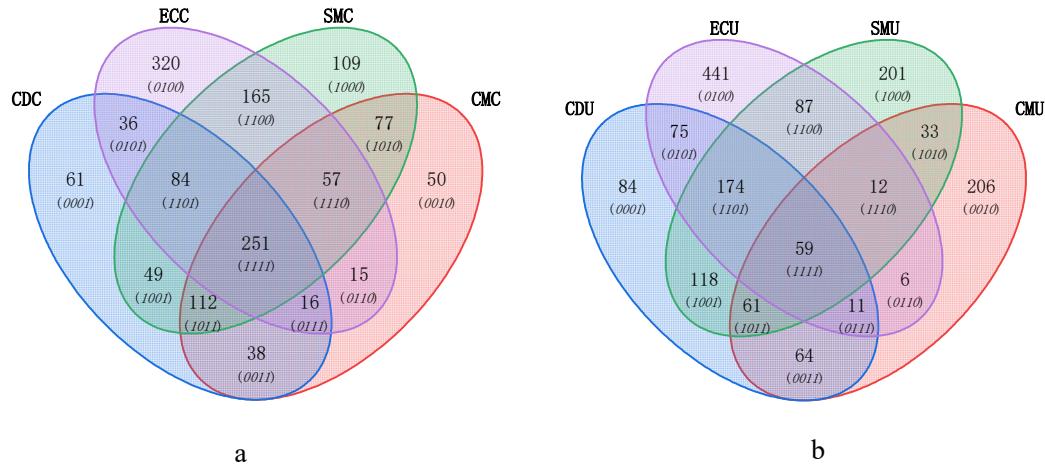


Figure S4. (a) Venn diagram showing the common and unique OTUs in organic fertilizer after composting. (b) Venn diagram showing the common and unique OTUs in uncomposted organic fertilizers. The binary-like numbers in the brackets in the figure indicate the inclusion relationship of different groups, 1 means include, 0 means not, and position indicates the group where it is located.

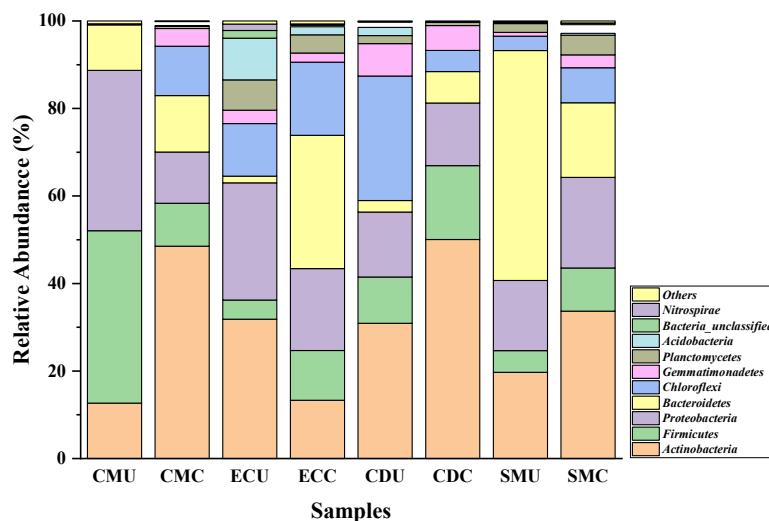


Figure S5. The effect of composting on the composition of organic fertilizer flora. Composition of the flora at the phylum level (mean, $n = 3$). Only the most abundant taxa (> 1% genus) are displayed (mean, $n = 3$).

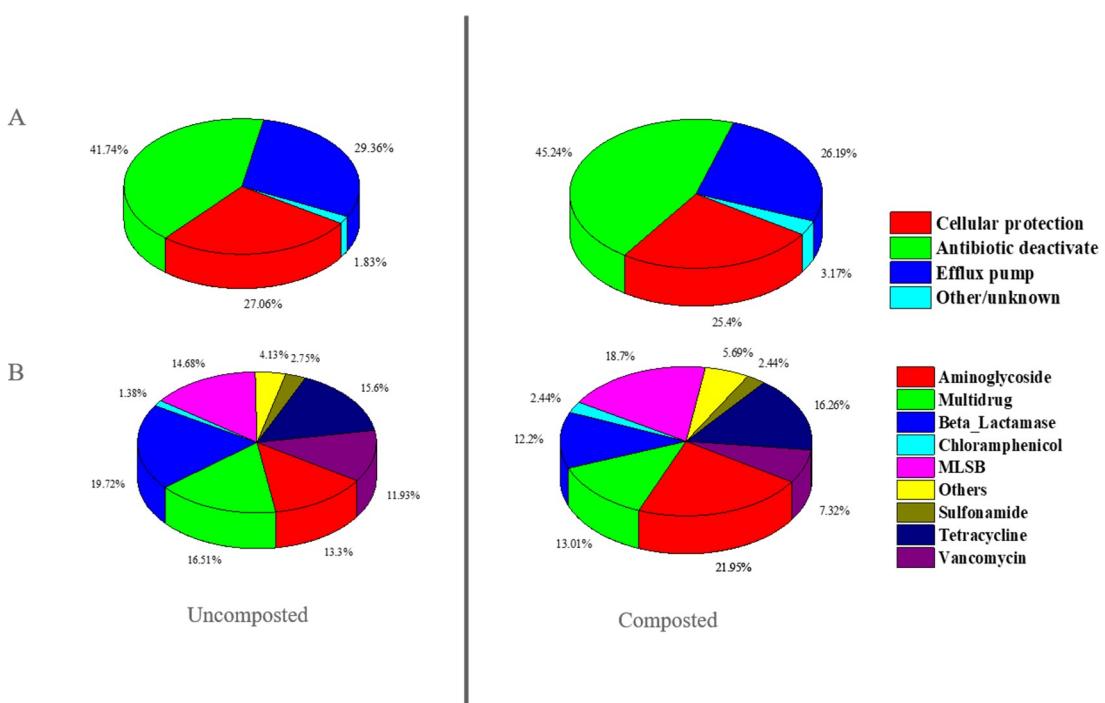


Figure S6. Resistance genes detected in all samples were classified based on (A) the mechanism of resistance and (B) the antibiotic to which they confer resistance. MLSB (Macrolide–Lincosamide–Streptogramin B).

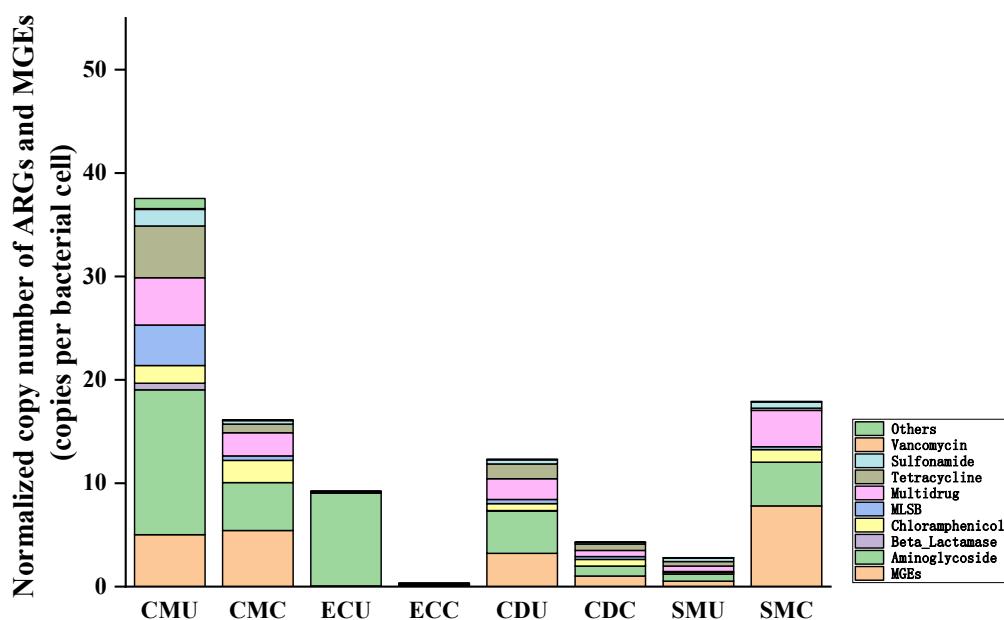


Figure S7. Normalized abundance of ARGs and MGE. Data shown in the figure are from three replicates and represented as the mean.

Table S1. Analysis of physicochemical properties.

Samples	C/N ratio	pH	NO ₃ ⁻ -N	NH ₄ ⁺ -N
CMU	5.35±0.54	7.36	13.77	53.71
CMC	7.04±0.62	7.59	13.99	53.20
ECU	9.97±0.41	6.92	14.07	6.07
ECC	9.92±0.06	6.79	14.04	4.14
CDU	9.14±0.40	7.35	13.81	41.10
CDC	8.58±0.53	6.85	14.17	54.30
SMU	10.49±0.85	7.26	14.11	9.36
SMC	8.94±0.49	7.01	14.15	4.97

Table S2. The tested 296 target genes in this study (MLSB = Macrolide-Lincosamide-Streptogramin B resistance).

#Gene Name	Forward Primer	Reverse Primer	Classification of Antibiotic Resistance	The Mechanism of Resistance
16S rRNA	GGGTTGCGCTCGTTGC	ATGGYTGTCGTCAAGCTCGTG		
aac	CCCTGCGTTGTGGCTATGT	TTGGCCACGCCAATCC	Aminoglycoside	antibiotic deactivate
aac(6')I1	GACCGGATTAAAGGCCGATG	CTTGCCTTGATATTCAAGTTTATAACCA	Aminoglycoside	antibiotic deactivate
aac(6')-Ib(aka aacA4)-01	GTTTGAGAGGCAAGGTACCGTAA	GAATGCCTGGCGTGTGTTGA	Aminoglycoside	antibiotic deactivate
aac(6')-Ib(aka aacA4)-02	CGTCGCCGAGCAACTTG	CGGTACCTTGCCTCTCAAACC	Aminoglycoside	antibiotic deactivate
aac(6')-Ib(aka aacA4)-03	AGAACGCACGCCGACACTT	GCTCTCATTCAAGCATTGCA	Aminoglycoside	antibiotic deactivate
aac(6')-II	CGACCCGACTCCGAACAA	GCACGAATCCTGCCTTCTCA	Aminoglycoside	antibiotic deactivate
aac(6')-Iy	GCTTGCGGATGCCTCAAT	GGAGAACAAAAATACCTCAAGGAAA	Aminoglycoside	antibiotic deactivate
aacA/aphD	AGAGCCTTGGGAAGATGAAGTT	TTGATCCATACCATAGACTATCTCATCA	Aminoglycoside	antibiotic deactivate
aacC	CGTCACTTATTCGATGCCCTAC	GTCGGGCGCGGCATA	Aminoglycoside	antibiotic deactivate
aacC1	GGTCGTGAGTTCGGAGACGTA	GCAAGTTCCCGAGGTAATCG	Aminoglycoside	antibiotic deactivate
aacC2	ACGGCATTCTCGATTGCTT	CCGAGCTTCACGTAAGCATT	Aminoglycoside	antibiotic deactivate
aacC4	CGGCGTGGGACACGAT	AGGGAACCTTGCCTCAACT	Aminoglycoside	antibiotic deactivate
aadA-01	GTTGTGCACGACGACATCATT	GGCTCGAAGATAACCTGCAAGAA	Aminoglycoside	antibiotic deactivate
aadA-02	CGAGATTCTCCCGCGCTGTA	GCTGCCATTCTCCAAATTGC	Aminoglycoside	antibiotic deactivate
aadA1	AGCTAAGCGCGAACTGCAAT	TGGCTCGAAGATAACCTGCAA	Aminoglycoside	antibiotic deactivate
aadA-1-01	AAAAGCCCGAAGAGGAACCTG	CATCTTCACAAAGATGTTGCTGTCT	Aminoglycoside	antibiotic deactivate
aadA-1-02	CGGAATTGAAAAAACTGATCGAA	ATACCGGCTGTCCGTCAATT	Aminoglycoside	antibiotic deactivate

aadA2-01	ACGGCTCCGCAGTGGAT	GGCCACAGTAACCAACAAATCA	Aminoglycoside	antibiotic deactivate
aadA2-02	CTTGTGTCATGACGACATC	TCGAAGATACCCGCAAGAATG	Aminoglycoside	antibiotic deactivate
aadA2-03	CAATGACATTCTGCGGGTATC	GACCTACCAAGGCAACGCTATG	Aminoglycoside	antibiotic deactivate
aadA5-01	ATCACGATCTTGCATTTGCT	CTGCGGATGGGCCTAGAAG	Aminoglycoside	antibiotic deactivate
aadA5-02	GTTCCTGCTTGCTCGCATT	GATGCTCGGCAGGCAAAC	Aminoglycoside	antibiotic deactivate
aadA9-01	CGCGGCAAGCCTATCTG	CAAATCAGCGACCGCAGACT	Aminoglycoside	antibiotic deactivate
aadA9-02	GGATGCACGCTTGGATGAA	CCTCTAGCGGCCGGAGTATT	Aminoglycoside	antibiotic deactivate
aadD	CCGACAACATTCTACCATCCTT	ACCGAACGCGCTCGTCGTATA	Aminoglycoside	antibiotic deactivate
aadE	TACCTTATTGCCCTTGGAAAGAGTTA	GGAACATATGTCCTTTAATTCTACAATCT	Aminoglycoside	antibiotic deactivate
acrA-01	CAACGATCGGACGGGTTTC	TGGCGATGCCACCGTACT	Multidrug	efflux pump
acrA-02	GGTCTATCACCCATCGCGCTATC	GCGCGCACGAACATACC	Multidrug	efflux pump
acrA-03	CAGACCCGCATCGCATATT	CGACAATTTCGCGCTCATG	Multidrug	efflux pump
acrA-04	TACTTGCAGGCCATCTTC	CGTGCAGAACGAAACAT	Multidrug	efflux pump
acrA-05	CGTGCAGAACGAAACA	ACTTGCAGGCCATCTTC	Multidrug	efflux pump
acrB-01	AGTCGGTGTTCGCCGTTAAC	CAAGGAAACGAACGCAATACC	Multidrug	efflux pump
acrF	GCGGCCAGGCACAAAAA	TACGCTCTCCACGGTTTC	Multidrug	efflux pump
acrR-01	GCGCTGGAGACACGACAAC	GCCTTGCTGCGAGAACAAA	Multidrug	efflux pump
acrR-02	GATGATACCCCCTGCTGTGAGA	ACCAAACAAGAACGCGAAGAA	Multidrug	efflux pump
adeA	CAGTCGAGCGCTATTCTG	CGCCCTGACCGACCAAT	Multidrug	efflux pump
ampC/blaDHA	TGGCCGCAGCAGAAAGA	CCGTTTATGCACCCAGGAA	Beta_Lactamase	antibiotic deactivate
ampC-01	TGGCGTATCGGGTCAATGT	CTCCACGGGCCAGTTGAG	Beta_Lactamase	antibiotic deactivate
ampC-02	GCAGCACGCCCGTAA	TGTACCCATGATGCGCGTACT	Beta_Lactamase	antibiotic deactivate
ampC-04	TCCGGTGACGCGACAGA	CAGCACGCCGGTGAAGT	Beta_Lactamase	antibiotic deactivate
ampC-05	CTGTTCGAGCTGGTTCTATAAGTAAA	CAGTATCTGGTCACCGGATCGT	Beta_Lactamase	antibiotic deactivate
ampC-06	CCGCTCAAGCTGGACCATAC	CCATATCCTGCACGTTGGTT	Beta_Lactamase	antibiotic deactivate

ampC-07	CCGCCAGAGCAAGGACTA	GCTCGACTTCACGCCGTAG	Beta_Lactamase	antibiotic deactivate
ampC-09	CAGCGCTGATGAAAAATATG	CAGCGAGCCCACCTCGA	Beta_Lactamase	antibiotic deactivate
aph	TTTCAGCAAGTGGATCATGTTAAAAT	CCAAGCTTTCCACTGTTTTC	Aminoglycoside	antibiotic deactivate
aph(2')-Id-01	TGAGCAGTATCATAAGTTGAGTGAAAG	GACAGAACATCAATCTCTATGGAATG	Aminoglycoside	antibiotic deactivate
aph(2')-Id-02	TAAGGATATACCGACAGTTGGAAA	TTTAATCCCTTTCATACCAATCCATA	Aminoglycoside	antibiotic deactivate
aph6ia	CCCATCCCATGTGTAAGGAAA	GCCACCGCTCTGCTGTAC	Aminoglycoside	antibiotic deactivate
aphA1(aka kanR)	TGAACAAGTCTGGAAAGAAATGCA	CCTATTAAATTCCCCCTCGTAAAAA	Aminoglycoside	antibiotic deactivate
bacA-01	CGGCTTCGTGACCTCGTT	ACAATGCGATACCAGGCAAAT	Others	antibiotic deactivate
bacA-02	TTCCACGACACGATTAAGTCATTG	CGGCTTTCGGCTTCAG	Others	antibiotic deactivate
bla1	GCAAGTTGAAGCGAAAGAAAAGA	TACCAAGTATCAATCGCATATACACCTAA	Beta_Lactamase	antibiotic deactivate
bla-ACC-1	CACACAGCTGATGGCTTATCTAAAA	AATAAACCGCGATGGGTTCCA	Beta_Lactamase	antibiotic deactivate
blaCMY	CCGGCGGAAATTAAGC	GCCACTGTTGCCTGTCAGTT	Beta_Lactamase	antibiotic deactivate
blaCMY2-01	AAAGCCTCAT GGGTCATAAA	ATAGCTTTGTTGCCAGCATCA	Beta_Lactamase	antibiotic deactivate
blaCMY2-02	GCGAGCAGCCTGAAGCA	CGGATGGGCTTGTCCCTTT	Beta_Lactamase	antibiotic deactivate
blaCTX-M-01	GGAGGCGTGACGGTTTT	TTCAGTGCATCCAGACGAA	Beta_Lactamase	antibiotic deactivate
blaCTX-M-02	GCCGCGGTGCTGAAGA	ATCGGATTATAGTTAACCAAGGTCAGATT	Beta_Lactamase	antibiotic deactivate
blaCTX-M-03	CGATACCACCAACGCCGTTA	GCATTGCCAACGTCAGATT	Beta_Lactamase	antibiotic deactivate
blaCTX-M-04	CTTGGCGTTGCGCTGAT	CGTTCATGGCACGGTAGA	Beta_Lactamase	antibiotic deactivate
blaCTX-M-05	GCGATAACGTGGCGATGAAT	GTCGAGACGGAACGTTTCGT	Beta_Lactamase	antibiotic deactivate
blaCTX-M-06	CACAGTTGGTGACGTGGCTTAA	CTCCGCTGCCGGTTTATC	Beta_Lactamase	antibiotic deactivate
blaGES	GCAATGTGCTAACGTTCAAG	GTGCCTGAGTCATTCTTCAAAG	Beta_Lactamase	antibiotic deactivate

blaIMP-01	AACACGGTTGGTGGTTCTTGTAA	GCGCTCCACAAACCAATTG	Beta_Lactamase	antibiotic deactivate
blaIMP-02	AAGGCAGCATTCCCTCTCATTTT	GGATAGATCGAGAATTAAGCCACTCT	Beta_Lactamase	antibiotic deactivate
bla-L1	CACCGGGTACCAAGCTGAAG	GCGAAGCTGCGCTTGTAGTC	Beta_Lactamase	antibiotic deactivate
blaMOX/blaCMY	CTATGTCAATGTGCCGAAGCA	GGCTTGCTCTTTCGAACATAGC	Beta_Lactamase	antibiotic deactivate
blaOCH	GGCGACTTGC CGCGTAT	TTTCTGCTCGGCCATGAG	Beta_Lactamase	antibiotic deactivate
blaOKP	GCCGCCATCACCATGAG	GGTGACGTTGTCACCGATCTG	Beta_Lactamase	antibiotic deactivate
blaOXA1/blaOXA30	CGGATGGTTGAAGGGTTATTAT	TCTTGGCTTTATGCTTGATGTTAA	Beta_Lactamase	antibiotic deactivate
blaOXA10-01	CGCAATTATCGGCCTAGAAA	TTGGCTTCCGTCCCATT	Beta_Lactamase	antibiotic deactivate
blaOXA10-02	CGCAATTATCGGCCTAGAAA	TTGGCTTCCGTCCCATT	Beta_Lactamase	antibiotic deactivate
blaOXY	CGTTCAGGCAGGTT	GCCCGATATAAGATTGAGAATT	Beta_Lactamase	antibiotic deactivate
blaPAO	CGCCGTACAACCGGTGAT	GAAGTAATGCGTTCTCCTTCA	Beta_Lactamase	antibiotic deactivate
blaPER	TGCTGGTTGCTTTTGTA	CCTGCATGATAGCTTCAT	Beta_Lactamase	antibiotic deactivate
blaPSE	TTGTGACCTATTCCCTGTAATAGAA	TGCGAACGCACGCATCATC	Beta_Lactamase	antibiotic deactivate
blaROB	GCAAAGGCATGACGATTGC	CGCGCTGTTGTCGCTAAA	Beta_Lactamase	antibiotic deactivate
blaSFO	CCGCCGCATCCAGTA	GGGCCGCCAAGATGCT	Beta_Lactamase	antibiotic deactivate
blaSHV-01	TCCCATGATGAGCACCTTAAA	TTCGTACCGGGCATCCA	Beta_Lactamase	antibiotic deactivate
blaSHV-02	CTTTCCCATGATGAGCACCTT	TCCTGCTGGCGATAGTGGAT	Beta_Lactamase	antibiotic deactivate
blaTEM	AGCATCTTACGGATGGCATGA	TCCTCCGATCGTTGTCAGAAGT	Beta_Lactamase	antibiotic deactivate
blaTLA	ACACTTGCCATTGCTGTTATGT	TGCAAATTCCGGCAATAATCTT	Beta_Lactamase	antibiotic deactivate
blaVEB	CCCGATGCAAAGCGTTATG	GAAAGATTCCCTTATCTATCTCAGACAA	Beta_Lactamase	antibiotic deactivate
blaVIM	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT	Beta_Lactamase	antibiotic deactivate
blaZ	GGAGATAAAAGTAACAAATCCAGTTAGATATGA	TGCTTAATTCCATTGCGATAAG	Beta_Lactamase	antibiotic deactivate

carB	GGAGTGAGGCTGACCGTAGAAG	ATCGGCGAACGCACAAA	MLSB	efflux pump
catA1	GGGTGAGTTCACCAAGTTGATT	CACCTTGTGCGCTTGCCTATA	Others	antibiotic deactivate
catB3	GCACTCGATGCCCTCCAAAA	AGAGCCGATCCAACGTCAT	Others	antibiotic deactivate
catB8	CACTCGACGCCCTCCAAAG	CCGAGCCTATCCAGACATCATT	Others	antibiotic deactivate
ceoA	ATCAACACGGACCAGGACAAG	GGAAAGTCCGCTCACGATGA	Multidrug	efflux pump
cepA	AGTTGCGCAGAACAGTCCTT	TCGTATCTTGCCGTCGATAAT	Beta_Lactamase	antibiotic deactivate
cfiA	GCAGCGTTGCTGGACACA	GTTGGGATAAACGTGGTGA	Beta_Lactamase	antibiotic deactivate
cfr	GCAAAATTCAAGAGCAAGTTACGAA	AAAATGACTCCAACCTGCTTTAT	Others	antibiotic deactivate
cfxA	TCATTCCCTCGTTCAAGTTTCAGA	TGCAGCACCAAGAGGAGATGT	Beta_Lactamase	antibiotic deactivate
cIntI-1(class1)	GGCATCCAAGCAGCAAG	AAGCAGACTTGACCTGA	Integron	integrase
cmeA	GCAGCAAAGAAGAACCAAA	AGCAGGGTAAGTAAACTAACGTGGAAATCT	Multidrug	efflux pump
cmlA1-01	TAGGAAGCATCGAACGTTGAT	CAGACCGAGCACGACTGTTG	Chloramphenicol	efflux pump
cmlA1-02	AGGAAGCATCGAACGTTGA	ACAGACCGAGCACGACTGTTG	Chloramphenicol	efflux pump
cmr	CGGCATCGTCAGTGGATT	CGGTTCCGAAAAAGATGGAA	Multidrug	efflux pump
cmx(A)	GCGATGCCATCCTCTGT	TCGACACGGAGCCTTGGT	Chloramphenicol	efflux pump
cphA-01	GCGAGCTGCACAAGCTGAT	CGGCCAGTCGCTCTTC	Beta_Lactamase	antibiotic deactivate
cphA-02	GTGCTGATGGCGAGTTCTG	GGTGTGGTAGTTGGTGTGATCAC	Beta_Lactamase	antibiotic deactivate
dfrA1	GGAATGGCCCTGATATTCCA	AGTCTTGTGCTCCAACCAACAG	Sulfonamide	antibiotic deactivate
dfrA12	CCTCTACCGAACCGTCACACA	GCGACAGCGTTGAAACAACCTAC	Sulfonamide	antibiotic deactivate
emrD	CTCAGCAGTATGGTGGTAAGCATT	ACCAGGCGCCGAAGAAC	Multidrug	efflux pump
ereA	CCTGTGGTACGGAGAACATTGATGT	ACCGCATTGCTTTGCTT	MLSB	antibiotic deactivate
ereB	GCTTATTTCAGGAGGCAGAAT	TTTTAAATGCCACAGCACAGAAC	Others	antibiotic deactivate

erm(34)	GCGCGTTGACGACGATT	TGGTCATACTCGACGGCTAGAAC	MLSB	cellular protection
erm(35)	TTGAAAACGATGTTGCATTAAGTCA	TCTATAATCACAACTAACCACCTGAACGT	MLSB	cellular protection
erm(36)	GGCGGACCGACTTGCAT	TCTGCGTTGACGACGGTTAC	MLSB	cellular protection
ermA	TTGAGAAGGGATTGCGAAAAG	ATATCCATCTCCACCATTAATAGTAAACC	MLSB	cellular protection
ermA/ermTR	ACATTTACCAAGGAACTTGTGGAA	GTGGCATGACATAAACCTTCATCA	MLSB	cellular protection
ermB	TAAAGGGCATTAAACGACGAAACT	TTTATACCTCTGTTGTTAGGAAATTGAA	MLSB	cellular protection
ermC	TTTGAAATCGGCTCAGGAAAA	ATGGTCTATTCAATGGCAGTTACG	MLSB	cellular protection
ermF	CAGCTTGGTGAACATTACGAA	AAATTCTAAAATCACAACCGACAA	MLSB	cellular protection
ermJ/ermD	GGACTCGGCAATGGTCAGAA	CCCCGAAACGCAATATAATGTT	MLSB	cellular protection
ermK-01	GTTTGATATTGGCATTGTCAGAGAAA	ACCATTGCCGAGTCCACTTT	MLSB	cellular protection
ermK-02	GAGCCGCAAGCCCCTT	GTGTTTCATTGACGCGGAGTAA	MLSB	cellular protection
ermT-01	GTTCACTAGCACTATTTTAATGACAGAAAGT	GAAGGGTGTCTTTTAATACAATTAACGA	MLSB	cellular protection
ermT-02	GTAAAATCCCTAGAGAATACTTCATCCA	TGAGTGATATTTGAAGGGTGTCTT	MLSB	cellular protection
ermX	GCTCAGTGGTCCCCATGGT	ATCCCCCCGTCAACGTTT	MLSB	cellular protection
ermY	TTGTCTTGAAAGTGAAGCAACAGT	TAACGCTAGAGAACGATTGTATTGAG	MLSB	cellular protection
fabK	TTTCAGCTCAGCACTTGGTCAT	AAGGCATTTTCAGCCAGTTC	Others	antibiotic deactivate
floR	ATTGTCTTCACGGTGTCCGTTA	CCCGCGATGTCGTCGAACT	Multidrug	efflux pump
folA	CGAGCAGTTCTGCCAAAG	CCCAGTCATCCGGTTCATATC	Sulfonamide	antibiotic deactivate
fosB	TCACTGTAACATAATGAAGCATTAGACCAT	CCATCTGGATCTGAAAGTAAAGAGATC	Others	antibiotic deactivate
fosX	GATTAAGCCATATCACTTAATTGTGAAAG	TCTCCTTCATAATGCAAATCCA	Others	antibiotic deactivate

fox5	GGTTTGCCGCTGCAGTTC	GCGGCCAGGTGACCAA	Beta_Lactamase	antibiotic deactivate
imiR	CCGGACTAGAGCTTCATGTAAGC	CCCACGCGGTACTCTGTAAA	Others	other/unknown
intl-1(clinic)	CGAACGAGTGGCGGAGGGTG	TACCCGAGAGCTTGGCACCCA	Integron	integrase
IS613	AGGTTCGGACTCAATGCAACA	TTCAGCACATACCGCCTTGAT	Transposase	transposase
lmrA-01	TCGACGTGACCGTAGTGAACA	CGTGAECTACCCAGGTGAGTTGA	MLSB	efflux pump
lnuA-01	TGACGCTCAACACACTCAAAAA	TTCATGCTTAAGTCCATACGTGAA	MLSB	antibiotic deactivate
lnuB-01	TGAACATAATCCCCTCGTTAAAGAT	TAATTGCCCTGTTCATCGTAAATAA	MLSB	antibiotic deactivate
lnuB-02	AAAGGAGAAGGTGACCAATACTCTGA	GGAGCTACGTCAAACAAACCAGTT	MLSB	antibiotic deactivate
lnuC	TGGTCATATAACAGATGTAACCAAGATT	CACCCCCAGGCCACCATCAA	MLSB	antibiotic deactivate
marR-01	GCGCGTACTGGTGAAGCTA	TGCCCTGGTCGTTGATGA	Multidrug	efflux pump
matA/mel	TAGTAGGCAAGCTCGGTGTTGA	CCTGTGCTATTTAACGCCTGTTCT	MLSB	efflux pump
mdetII	ATACAGCAGTGGATATTGGTTAATTGT	TGCATAAGGTGAATGTTCCATGA	Multidrug	efflux pump
mdtA	CCTAACGGGCGTGACTTCA	TTCACCTGTTCAAGGGTCAA	MLSB	efflux pump
mdtE/yhiU	CGTCGGCGCACTCGTT	TCCAGACGTTGTACGGTAACCA	Multidrug	efflux pump
mecA	GGTTACGGACAAGGTGAAATACTGAT	TGTCTTTAATAAGTGAGGTGCGTTAATA	Beta_Lactamase	cellular protection
mefA	CCGTAGCATTGGAACAGCTTT	AAACGGAGTATAAGAGTGCTGCAA	MLSB	efflux pump
mepA	ATCGGTGCGCTTTCGTTCAC	ATAAAATAGGATCGAGCTGCTGGAT	Multidrug	efflux pump
mexA	AGGACAACGCTATGCAACGAA	CCGGAAAGGGCCGAAAT	Multidrug	efflux pump
mexD	TTGCCACTGGCTTCATGAG	CACTCGGGAGAACTGCTGTAGA	Multidrug	efflux pump
mexE	GGTCAGCACCAGACAAGGTCTAC	AGCTCGACGTACTTGAGGAACAC	Multidrug	efflux pump
mexF	CCGCGAGAAGGCCAAGA	TTGAGTTCGGCGGTGATGA	Multidrug	efflux pump

mphA-01	CTGACGCCTCCGTGTT	GGTGGTGCATGGCGATCT	MLSB	antibiotic deactivate
mphA-02	TGATGACCCGCCATCGA	TTCGCAGCCCCCTCTC	MLSB	antibiotic deactivate
mphB	CGCAGCGCTTGATCTGTAG	TTACTGCATCCATACGCTGCT	MLSB	antibiotic deactivate
mphC	CGTTGAAGTACCGAATTGGAAA	GCTCGGGTTTGCGCTGTA	MLSB	antibiotic deactivate
msrA-01	CTGCTAACACAAGTACGATTCAAAT	TCAAGTAAAGTTGCTTACCTACACCATT	MLSB	efflux pump
msrC-01	TCAGACCGGATCGGTTGTC	CCTATTTTGAGTCTCTCTAATGTT	MLSB	efflux pump
mtrC-01	GGACGGGAAGATGGTCAA	CGTAGCGTCCGGTTCGAT	Multidrug	efflux pump
mtrC-02	CGGAGTCCATCGACCATTG	ATCGTCGGCAAGGAGAACATCA	Multidrug	efflux pump
mtrD-02	GGTCGGCACGCTCTGTC	TGAAGAATTGCGCACCACTAC	Multidrug	efflux pump
mtrD-03	CCGCCAACCGATATAAGACA	GGCCGGGTTGCCAAA	Multidrug	efflux pump
ndm-1	ATTAGCCGCTGCATTGAT	CATGTGAGATAGGAAGTG	Beta_Lactamase	antibiotic deactivate
nimE	TGCGCCAAGATAGGGCATA	GTCGTGAATTCGGCAGGTTA	Others	other/unknown
nisB	GGGAGAGTTGCCGATTTGTA	AGCCACTCGTAAAGGGCAAT	Others	other/unknown
oleC	CCCGGAGTCGATGTTCGA	GCCGAAGACGTACACGAACAG	MLSB	efflux pump
oprD	ATGAAGTGGAGCGCCATTG	GGCACGGCGAACTGA	Multidrug	efflux pump
oprJ	ACGAGAGTGGCGTCGACAA	AAGGCGATCTCGTTGAGGAA	Multidrug	efflux pump
pbp	CCGGTGCCATTGGTTAGA	AAAATAGCCGCCCAAGATT	Beta_Lactamase	cellular protection
pbp2x	TTTCATAAGTATCTGGACATGGAAGAA	CCAAAGGAAACTTGCTTGAGATTAG	Beta_Lactamase	cellular protection
Pbp5	GGCGAACTTCTAATTAATCCTATCCA	CGCCGATGACATTCTTCTTATCTT	Beta_Lactamase	cellular protection
penA	AGACGGTAACGTATAACTTTGAAAGA	GCGTAGCCGGCAATG	Beta_Lactamase	cellular protection
pikR1	TCGACATGCGTGACGAGATT	CCGCGAATTAGGCCAGAA	MLSB	cellular protection
pikR2	TCGTGGGCCAGGTGAAGA	TTCCCCTGCCGGTGAA	MLSB	cellular protection
pmra	TTTGCAGGTTTGTCCCTAATGC	GCAGAGCCTGATTCTCCTTG	Multidrug	efflux pump

pncA	GCAATCGAGGCGGTGTC	TTGCCGCAGCCAATTCA	Others	other/unknown
putitive multidrug	AATTTGCCGATTATTGCTGAAA	GATTGTCATCATTGTTATCACCAA	Multidrug	efflux pump
qac	CAATAATAACCGAAATAATAGGGACAAGTT	AATAAGTGTCCCTAGTGTTGGCCATAG	Multidrug	efflux pump
qacA	TGGCAATAGGAGCTATGGTGT	AAGGTAACACTATTTCGGTCAAATC	Multidrug	efflux pump
qacA/qacB	TTTAGGCAGCCTCGCTTCA	CCGAATCCAATAAAACCCAATAA	Multidrug	efflux pump
qacEdelta1-01	TCGCAACATCCGCATTTAAA	ATGGATTCAGAACAGAGAAAGAAA	Multidrug	efflux pump
qacEdelta1-02	CCCCTCCGCCGTTGT	CGACCAGACTGCATAAGCAACA	Multidrug	efflux pump
qacH-01	GTGGCAGCTATCGCTTGGAT	CCAACGAACGCCACAA	Multidrug	efflux pump
qacH-02	CATCGTGCTGTGGCAGCTA	TGAACGCCAGAAGTCTAGTTT	Multidrug	efflux pump
qnR	AGGATTCTCACGCCAGGATT	CCGCTTCATGAAACTGCAA	Others	other/unknown
rarD-02	TGACGCATCGCTGATCT	AAATTTCTGTGGCGTCTGAATC	Multidrug	efflux pump
sat4	GAATGGGCAAAGCATAAAAACTG	CCGATTGAAACCACAATTATGATA	Others	antibiotic deactivate
sdeB	CACTACCGCTTCCGCACTTAA	TGAAAAAACGGAAAAGTCAT	Multidrug	efflux pump
spcN-01	AAAAGTTCGATGAAACACGCCAT	TCCAGTGGTAGTCCCCGAATC	Aminoglycoside	antibiotic deactivate
spcN-02	CAGAATCTCCTGAAAAGTTGATGAA	CGCAGACACGCCGAATC	Aminoglycoside	antibiotic deactivate
speA	GCAAGAGGTATTGCTCAACAAGA	CAGGGTCACCCCTATAAGAAAA	Others	other/unknown
str	AATGAGTTTGGAGTGTCAACGTA	AATCAAAACCCCTATTAAAGCCAAT	Aminoglycoside	antibiotic deactivate
strA	CCGGTGGCATTTGAGAAAAAA	GTGGCTCAACCTGCGAAAAG	Aminoglycoside	antibiotic deactivate
strB	GCTCGGTGAGAACATCT	CAATTTCGGTCGCCTGGTAGT	Aminoglycoside	antibiotic deactivate
sull	CAGCGCTATCGCCTCAAG	ATCCCGCTGCGCTGAGT	Sulfonamide	cellular protection
sul2	TCATCTGCCAAACTCGTCGTTA	GTCAAAGAACGCCGAATGT	Sulfonamide	cellular protection

sulA/folP-01	CAGGCTCGTAAATTGATAGCAGAAG	CTTCCTTGCAGATCGCTTT	Sulfonamide	cellular protection
sulA/folP-03	CACGGCTTCGGCTCATGT	TGCCATCCTGTGACTAGCTACGT	Sulfonamide	cellular protection
tet(32)	CCATTACTTCGGACAACGGTAGA	CAATCTCTGTGAGGGCATTAAACA	Tetracycline	cellular protection
tet(34)	CTTAGCGCAAACAGCAATCAGT	CGGTGATACAGCGCGTAAACT	Tetracycline	other/unknown
tet(35)	ACCCCATGACGTACCTGTAGAGA	CAACCCACACTGGCTACCAGTT	Tetracycline	other/unknown
tet(36)-01	AGAATACTCAGCAGAGGTCAAGTCCT	TGGTAGGTCGATAACCCGAAAAT	Tetracycline	cellular protection
tet(36)-02	TGCAGGAAAGACCTCCATTACAG	CTTTGTCCACACTTCCACGTACTATG	Tetracycline	cellular protection
tet(37)	GAGAACGTTGAAAAGGTGGTGA	AACCAAGCCTGGATCAGTCTCA	Tetracycline	other/unknown
tetA-01	GCTGTTGTTCTGCCGGAAA	GGTTAAGTTCTTGAAACGCAAAC	Tetracycline	efflux pump
tetA-02	CTCACCAAGCCTGACCTCGAT	CACGTTGTTATAGAAGCCGCATAG	Tetracycline	efflux pump
tetB-01	AGTGCCTTGGATGCTGTA	AGCCCCAGTAGCTCCTGTGA	Tetracycline	efflux pump
tetB-02	GCCCAGTGTGTTGTTGTCAT	TGAAAGCAAACGGCCTAAATACA	Tetracycline	efflux pump
tetC-01	CATATCGCAATACATGCGAAAAA	AAAGCCGCGGTAAATAGCAA	Tetracycline	efflux pump
tetC-02	ACTGGTAAGGTAAACGCCATTGTC	ATGCATAAACCAAGCCATTGAGTAAG	Tetracycline	efflux pump
tetD-01	TGCCCGCTTGATTACACA	CACCAAGTGATCCCAGGAGATAA	Tetracycline	efflux pump
tetD-02	TGTCATCGCGCTGGTGATT	CATCCGCTTCCGGGAGAT	Tetracycline	efflux pump
tetE	TTGGCGCTGTATGCAATGAT	CGACGACCTATGCGATCTGA	Tetracycline	efflux pump
tetG-01	TCAACCATTGCCGATTCGA	TGGCCCGGCAATCATG	Tetracycline	efflux pump
tetG-02	CATCAGGCCGGTCTTATG	CCCCATGTAGCCGAACCA	Tetracycline	efflux pump
tetH	TTGGGTCACTTACCAAGCATTAA	TTGCGCATTATCATCGACAGA	Tetracycline	efflux pump
tetJ	GGGTGCCGCATTAGATTACCT	TCGTCCAATGTAGAGCATCCATA	Tetracycline	efflux pump

tetK	CAGCAGTCATTGGAAAATTATCTGATTATA	CCTTGTACTAACCTACCAAAAAATCAAATA	Tetracycline	efflux pump
tetL-01	AGCCCGATTATTCAAGGAATTG	CAAATGCTTCCCCCTGTTCT	Tetracycline	efflux pump
tetL-02	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT	Tetracycline	efflux pump
tetM-01	CATCATAGACACGCCAGGACATAT	CGCCATCTTGAGAAATCA	Tetracycline	cellular protection
tetM-02	TAATATTGGAGTTTAGCTCATGTTGATG	CCTCTCTGACGTTCTAAAAGCGTATTAT	Tetracycline	cellular protection
tetO-01	ATGTGGATACTACAACGCATGAGATT	TGCCTCCACATGATATTTTCCT	Tetracycline	cellular protection
tetPA	AGTTGCAGATGTGTAGTCGAAACTATCTA TT	TGCTACAAAGTACGAAAACAAACTAGAA	Tetracycline	efflux pump
tetPB-01	ACACCTGGACACGCTGATT	ACCGTCTAGAACCGCGGAATG	Tetracycline	cellular protection
tetPB-02	TGATACACCTGGACACGCTGAT	CGTCCAAAACGCGGAATG	Tetracycline	cellular protection
tetPB-03	TGGGCGACAGTAGGCTTAGAA	TGACCCTACTGAAACATTAGAAATACCT	Tetracycline	cellular protection
tetPB-04	AGTGGTGCAAATACTGAAAAAGTTGT	TTTGTTCCTTCGTTTGGACAGA	Tetracycline	cellular protection
tetPB-05	CTGAAGTGGAGCGATCATTCC	CCCTCAACGGCAGAAATAACTAA	Tetracycline	cellular protection
tetQ	CGCCTCAGAAGTAAGTCATACACTAAG	TCGTTCATGCGGATATTATCAGAAT	Tetracycline	cellular protection
tetR-02	CGCGATAGACGCCTTCGA	TCCTGACAACGAGCCTCCTT	Tetracycline	efflux pump
tetR-03	CGCGATGGAGCAAAAGTACAT	AGTAAAAACCTTGTGGCATAAAA	Tetracycline	efflux pump
tetS	TTAAGGACAAACTTCTGACGACATC	TGTCTCCCATTGTTCTGGTTCA	Tetracycline	cellular protection
tetT	CCATATAGAGGTTCCACCAATCC	TGACCTATTGGTAGTGGTTCTATTG	Tetracycline	cellular protection
tetU-01	GTGGCAAAGCAACGGATTG	TGCGGGCTTGCAAAACTATC	Tetracycline	other/unknown
tetV	GCGGGAACGACGATGTATATC	CCGCTATCTCACGACCATGAT	Tetracycline	efflux pump

tetX	AAATTGTTACCGACACGGAAGTT	CATAGCTGAAAAAATCCAGGACAGTT	Tetracycline	other/unknown
tnpA-01	CATCATCGGACGGACAGAAATT	GTCGGAGATGTGGGTGTAGAAAGT	Transposase	transposase
tnpA-02	GGGCGGGTCGATTGAAA	GTGGCAGGATCTGCTT	Transposase	transposase
tnpA-03	AATTGATGCGGACGGCTAA	TCACCAAACTGTTATGGAGTCGTT	Transposase	transposase
tnpA-04	CCGATCACGGAAAGCTCAAG	GGCTCGCATGACTTCGAATC	Transposase	transposase
tnpA-05	GCCGCACTGTCGATTTTATC	GCGGGATCTGCCACTTCTT	Transposase	transposase
tnpA-07	GAAACCGATGCTACAATATCCAATT	CAGCACCGTTGCAGTGTAAG	Transposase	transposase
tolC-01	GGCCGAGAACCTGATGCA	AGACTTACGCAATTCCGGGTTA	Multidrug	efflux pump
tolC-02	CAGGCAGAGAACCTGATGCA	CGCAATTCCGGGTTGCT	Multidrug	efflux pump
tolC-03	GCCAGGCAGAGAACCTGATG	CGCAATTCCGGGTTGCT	Multidrug	efflux pump
Tp614	GGAAATCAACGGCATCCAGTT	CATCCATGCGTTTGCTCT	Transposase	transposase
ttgA	ACGCCAATGCCAACGATT	GTCACGGCGCAGCTTGA	Multidrug	efflux pump
ttgB	TCGCCCTGGATGTACACCTT	ACCATTGCCACATCAACAAAC	Multidrug	efflux pump
vanA	AAAAGGCTCTGAAAACGCAGTTAT	CGGCCGTTATCTTGTAAAACAT	Vancomycin	cellular protection
vanB-01	TTGTCGGCGAAGTGGATCA	AGCCTTTTCCGGCTCGTT	Vancomycin	cellular protection
vanB-02	CCGGTCGAGGAACGAAATC	TCCTCCTGCAAAAAAAAGATCAAC	Vancomycin	cellular protection
vanC-01	ACAGGGATTGGCTATGAACCAT	TGACTGGCGATGATTGACTATG	Vancomycin	cellular protection
vanC-03	AAATCAATACTATGCCGGGCTTT	CCGACCGCTGCCATCA	Vancomycin	cellular protection
vanC1	AGGCGATAGCGGGATTGAA	CAATCGTCATTGCTATTCC	Vancomycin	cellular protection
vanC2/vanC3	TTTGAATGTCGGTGCCTGTGA	TCAATCGTTTCAGGCAATGG	Vancomycin	cellular protection
vanG	ATTTGAATTGGCAGGTATAACAGGTTA	TGATTGTCCTTGTCACATAATGC	Vancomycin	cellular protection
vanHB	GAGGTTCCGAGGCGACAA	CTCTCGGCGGCAGTCGTAT	Vancomycin	cellular protection
vanHD	GTGGCCGATTATACCGTCATG	CGCAGGTCATTCAAGGCAAT	Vancomycin	cellular protection

vanRA-01	CCCTTACTCCCACCGAGTTT	TTCGTCGCCCCATATCTCAT	Vancomycin	cellular protection
vanRA-02	CCACTCCGGCCTGTCAATT	GCTAACACATTCCCCCTGTTT	Vancomycin	cellular protection
vanRB	GCCCTGTCGGATGACGAA	TTACATAGTCGTCTGCCTCTGCAT	Vancomycin	cellular protection
vanRC	TGCGGGAAAAACTGAACGA	CCCCCCATACGGTTTGATTAA	Vancomycin	cellular protection
vanRC4	AGTGCTTGGCTTATCTGAAAA	TCCGGCAGCATCACATCTAA	Vancomycin	cellular protection
vanRD	TTATAATGGCAAGGATGCACTAAAGT	CGTCTACATCCGGAAGCATGA	Vancomycin	cellular protection
vanSA	CGCGTCATGCTTCAAATTCA	TCCGCAGAAAGCTCAATTGTT	Vancomycin	cellular protection
vanSB	GCGCGGCAAATGACAAC	TTTGCCTTTTATTGCACTGT	Vancomycin	cellular protection
vanSC-02	GCCATCAGCGAGTCTGATGA	CAGCTGGATCGTTTCCTT	Vancomycin	cellular protection
vanSE	TGGCCGAAGAAGCAGGAA	CAATAATACTCGTCAAAGGAGTTCTCA	Vancomycin	cellular protection
vanTC-01	CACACGCATTTCGCCATCTAG	CAGCCAACAGATCATCAAAACAA	Vancomycin	cellular protection
vanTC-02	ACAGTTGCCGCTGGTGAAG	CGTGGCTGGTCGATCAAAA	Vancomycin	cellular protection
vanTE	GTGGTGCCAAGGAAGTTGCT	CGTAGGCCACCGCAAAAAAAT	Vancomycin	cellular protection
vanTG	CGTGTAGCCGTTCCGTTCTT	CGGCATTACAGGTATATCTGGAAA	Vancomycin	cellular protection
vanWB	CGGACAAAGATACCCCCTATAAAG	AAATAGTAAATTGCTCATCTGGCACAT	Vancomycin	cellular protection
vanWG	ACATTTICATTTGGCAGCTTGAC	CCGCCATAAGAGCCTACAATCT	Vancomycin	cellular protection
vanXA	CGCTAAATATGCCACTTGGGATA	TCAAAAGCGATTCAGCCAACT	Vancomycin	cellular protection
vanXB	AGGCACAAAATCGAAGATGCTT	GGGTATGGCTCATCAATCAACTT	Vancomycin	cellular protection
vanXD	TAAACCGTGTATGGAACGAA	GCGATAGCCGTCCCATAAGA	Vancomycin	cellular protection
vanYB	GGCTAAAGCGGAAGCAGAAA	GATATCCACAGCAAGACCAAGCT	Vancomycin	cellular protection
vanYD-01	AAGGCATAACCTGACTGTCA	ATTGCCGGACGGAAGCA	Vancomycin	cellular protection
vanYD-02	CAAACGGAAGAGAGGTCACCTACA	CGGACGGTAATAGGGACTGTTC	Vancomycin	cellular protection

vatB-01	GGAAAAAGCAACTCCATCTCTTGA	TCCTGGCATAACAGTAACATTCTGA	MLSB	antibiotic deactivate
vatB-02	TTGGGAAAAGCAACTCCATCT	CAATCCACACATCATTCCAACA	MLSB	antibiotic deactivate
vatC-01	CGGAAATTGGAACGATGTT	GCAATAATAGCCCCGTTCTTA	MLSB	antibiotic deactivate
vatC-02	CGATGTTGGATTGGACGAGAT	GCTGCAATAATAGCCCCGTT	MLSB	antibiotic deactivate
vatE-01	GGTGCCATTATCGGAGCAAAT	TTGGATTGCCACCGACAAT	MLSB	antibiotic deactivate
vatE-02	GACCGTCCTACCAGGCGTAA	TTGGATTGCCACCGACAATT	MLSB	antibiotic deactivate
vgaA-01	CGAGTATTGTGGAAAGCAGCTAGTT	CCCGTACCGTTAGAGCCGATA	MLSB	efflux pump
vgaA-02	GACGGGTATTGTGGAAAGCAA	TTTCCTGTACCATTAGATCCGATAATT	MLSB	efflux pump
vgb-01	AGGGAGGGTATCCATGCAGAT	ACCAAATGCGCCCGTT	MLSB	efflux pump
vgbB-01	CAGCCGGATTCTGGTCCTT	TACGATCTCCATTCAATTGGGTAAA	MLSB	antibiotic deactivate
vgbB-02	ATACGAGCTGCTAATAAAGGATCTT	TGTGAACCACAGGGCATTATCA	MLSB	antibiotic deactivate
yeeE/mdtG-01	TGGCACAAAATATCTGGCAGTT	TTGTGTGGCGATAAGAGCATTAG	Multidrug	efflux pump
yeeE/mdtG-02	TTATCTGTTTCTGCTCACCTCTTTT	GCGTGGTGACAAACAGGGCTTA	Multidrug	efflux pump
yeeL/mdtH-01	TCGGGATGGTGGGCAAT	CGATAACCGAGCCGATGTAGA	Multidrug	efflux pump
yeeL/mdtH-02	CGCGTGAACCTTAAGTGCTT	AGACGGCTAAACCCATATAGCT	Multidrug	efflux pump
yeeL/mdtH-03	CTGCCGTTAAATGGATGTATGC	ACTCCAGCAGGGCGATAGG	Multidrug	efflux pump
yidY/mdtL-01	GCAGTTGCATATCGCCTTCTC	CTTCCCAGCAACAGCAT	Multidrug	efflux pump
yidY/mdtL-02	TGCTGATCAGGGATTCTGATTG	CAGGCCGACGAACATAAT	Multidrug	efflux pump

Table S3. Log number of Normalized gene copy numbers (copies per cell) (-: not detected).

#Gene Name	CMU	CMC	ECU	ECC	CDU	CDC	SMU	SMC
aac(6')-Ib(aka aacA4)-01	-1.14402	-2.39622	-4.08822	-	-1.73622	-2.42522	-2.78422	-2.27922
aac(6')-Ib(aka aacA4)-02	-0.82002	-2.21522	-	-3.81222	-1.70822	-2.30822	-2.88522	-2.14122
aac(6')-Ib(aka aacA4)-03	-1.06002	-2.13922	-3.86922	-3.62022	-1.54922	-2.15022	-2.65622	-2.09822
aac(6')-II	-1.22202	-2.84022	-	-4.33422	-2.01422	-	-3.25722	-
aacA/aphD	-	-2.72522	-4.20222	-	-2.54522	-3.15222	-3.44922	-2.82222
aacC	-	-	-3.83922	-	-	-	-	-
aacC1	-5.15202	-	-	-	-4.15722	-	-	-
aacC2	-1.13802	-3.66472	-3.66822	-	-3.14022	-3.93222	-3.41622	-3.70722
aacC4	-1.81902	-3.58822	-	-	-2.89522	-4.06522	-4.21322	-
aadA-01	-0.65802	-1.40322	-3.44622	-2.85522	-1.09722	-2.03622	-1.77022	-1.12822
aadA-02	-0.49902	-1.11222	-3.22722	-2.54322	-0.89622	-1.85022	-1.56622	-0.94822
aadA1	-0.31602	-0.88122	-3.00522	-2.58822	-0.89822	-1.54322	-1.55022	-0.65822
aadA-1-01	-0.76902	-1.99322	-3.89022	-3.44322	-2.52322	-2.79922	-4.12422	-
aadA-1-02	-	-1.73122	0.25278	-	-2.02122	-2.24122	-3.60622	-1.65522
aadA2-01	-0.89502	-1.03722	-3.92622	-3.02622	-1.28222	-1.66622	-2.09222	-0.81072
aadA2-02	-1.02702	-1.12322	-3.54822	-	-1.33022	-1.74622	-2.09722	-
aadA2-03	-0.54402	-0.81822	-3.30522	-2.57022	-0.79622	-1.46522	-1.54522	-
aadA5-01	-1.01202	-1.71822	-4.02822	-3.27222	-1.71822	-2.36922	-2.43722	-1.77522
aadA5-02	-1.21902	-1.72522	-	-3.05022	-1.63222	-2.18922	-2.37022	-1.65122
aadA9-01	-1.64802	-1.16322	-	-3.33222	-2.05822	-2.43322	-3.13022	-0.99522
aadA9-02	-1.87002	-1.31122	-3.87222	-3.53322	-2.20422	-2.49622	-3.23222	-1.38622
aadD	-1.04502	-1.03022	-3.85122	-3.71922	-1.84122	-2.72122	-3.06722	-1.57022

aadE	-1.08102	-1.33322	-3.22422	-3.33522	-1.70022	-1.71922	-3.10822	-1.79122
aph(2')-Id-01	-3.55002	-	-	-	-3.82122	-4.20622	-4.42922	-
aph(2')-Id-02	-2.37402	-3.78522	-	-	-3.36822	-4.09622	-	-3.58222
aphA1(aka kanR)	-0.88602	-2.82222	-	-4.04022	-2.14322	-3.02722	-	-2.21472
str	-	-3.20622	-	-4.69122	-3.43622	-3.81022	-3.77422	-3.91022
strA	-2.35302	-3.38822	-	-4.63122	-3.33522	-	-4.20822	-3.99672
strB	-0.84702	-1.98322	-3.19722	-3.29022	-1.47222	-2.75022	-2.69822	-2.03622
ampC/blaDHA	-2.78202	-	-	-	-3.73272	-	-	-4.58922
ampC-01	-4.25802	-	-	-	-	-	-	-4.52322
ampC-02	-2.26902	-	-	-	-	-	-4.28372	-
ampC-04	-4.97202	-	-3.94122	-	-	-4.06822	-4.05722	-
ampC-05	-4.40202	-	-	-	-4.08072	-	-	-
ampC-06	-4.77402	-	-	-	-4.08822	-	-	-
ampC-07	-5.66502	-	-	-	-	-	-	-
bla1	-	-	-4.03722	-3.34422	-	-	-	-
blaCMY	-3.30702	-	-	-	-	-	-	-
blaCMY2-01	-3.64002	-	-	-	-	-	-	-
blaCMY2-02	-5.11902	-	-	-	-	-	-	-4.77922
blaCTX-M-01	-2.78802	-	-	-	-	-	-	-
blaCTX-M-02	-2.55702	-	-4.53222	-	-	-	-	-
blaCTX-M-04	-	-	-3.31722	-	-4.22622	-	-4.21322	-
blaCTX-M-05	-2.78802	-	-	-	-	-	-	-
blaCTX-M-06	-4.57902	-	-	-	-	-	-	-
blaGES	-	-	-	-	-	-	-	-
blaMOX/blaCMY	-4.30302	-	-	-	-	-	-	-
blaOXA1/blaOXA30	-1.86402	-	-	-	-3.55522	-	-	-

blaOXA10-01	-1.65702	-	-4.11822	-	-3.44722	-4.04422	-4.19322	-
blaOXA10-02	-1.67502	-	-4.01622	-	-3.46422	-4.28722	-3.94322	-
blaOXY	-4.37802	-	-3.77622	-	-3.05022	-	-	-
blaPAO	-4.81602	-	-	-	-3.81322	-	-	-
blaPER	-2.26302	-	-	-	-	-	-	-
blaPSE	-1.64202	-	-4.38822	-	-3.20622	-4.15822	-4.07322	-
blaROB	-5.39502	-	-	-	-	-	-	-
blaSFO	-	-	-	-3.88422	-3.61222	-3.16522	-3.75272	-
blaSHV-01	-3.51402	-	-	-	-	-	-	-
blaSHV-02	-3.70902	-	-	-	-4.13022	-	-	-
blaTEM	-1.92402	-	-	-	-3.79722	-	-4.03422	-
blaVEB	-2.70702	-	-	-	-	-	-	-
blaVIM	-4.73502	-	-	-	-	-	-	-
blaZ	-3.92502	-	-	-	-	-	-	-4.76022
cepA	-4.68102	-	-	-	-	-	-	-
cfiA	-5.50302	-	-	-	-	-	-	-
cfxA	-2.52102	-	-	-4.88022	-4.33422	-	-	-4.76322
cphA-01	-	-	-3.45222	-	-3.19122	-	-3.96872	-
cphA-02	-	-	-	-	-	-4.01622	-	-
fox5	-	-	-2.82522	-	-3.01822	-3.33172	-3.09722	-
ndm-1	-	-	-	-	-	-	-	-4.66722
mecA	-4.21302	-	-	-	-	-	-	-
pbp	-2.93502	-	-	-	-	-	-	-
Pbp5	-1.92702	-	-	-	-4.05072	-	-	-4.27522
cmlA1-01	-2.17902	-2.35822	-4.15722	-4.20522	-2.31822	-3.23872	-2.02822	-2.16622
cmlA1-02	-2.13402	-2.32922	-	-4.16322	-2.21422	-3.05422	-1.91022	-2.09722

cmx(A)	-0.48702	-0.37622	-2.90922	-2.46522	-0.90522	-0.89722	-2.05622	-0.64222
ereA	-2.69202	-	-4.29222	-	-3.50522	-4.24222	-	-
lnuA-01	-	-	-4.59822	-	-4.06022	-	-3.53022	-3.87522
lnuB-01	-1.11702	-2.82222	-2.74722	-2.77422	-2.22622	-2.54222	-3.73822	-2.93222
lnuB-02	-1.51302	-3.40022	-3.11922	-3.23022	-2.68422	-2.94522	-4.19522	-3.36722
mphA-01	-	-	-	-	-	-3.83122	-3.94322	-
mphA-02	-	-	-	-	-2.79822	-	-	-
vatB-02	-	-	-	-	-	-	-	-
vatC-01	-5.57202	-	-4.08522	-4.90722	-4.14622	-	-	-4.95672
vatE-01	-1.37502	-3.56322	-3.88722	-4.77222	-3.77722	-3.70422	-4.45422	-4.52522
vatE-02	-1.75602	-3.77872	-	-	-3.77322	-3.91722	-	-
vgbB-01	-	-	-	-	-	-	-4.41722	-
vgbB-02	-5.49702	-	-	-	-	-4.29322	-	-
erm(34)	-	-	-	-	-3.76722	-	-	-
erm(35)	-2.29302	-3.48772	-	-	-3.16272	-	-4.49622	-3.05522
erm(36)	-2.41602	-2.62622	-4.19322	-	-2.37322	-3.66822	-4.02922	-
ermA	-1.76502	-2.06222	-	-	-2.73222	-3.13222	-	-
ermA/ermTR	-3.85902	-	-	-	-	-	-	-
ermB	-	-2.35922	-4.47822	-	-2.67822	-3.60422	-3.60422	-2.67522
ermC	-2.09502	-2.21922	-	-	-2.81222	-3.50422	-4.11322	-
ermF	-0.44502	-1.59722	-4.16322	-3.64122	-1.66322	-2.28122	-1.98722	-1.53672
ermJ/ermD	-5.40402	-	-	-	-3.56222	-4.28872	-4.28522	-
ermK-01	-	-	-	-	-3.60522	-	-	-
ermT-01	-1.25802	-2.75522	-	-4.41522	-2.24922	-3.27422	-3.19322	-2.82672
ermT-02	-1.15902	-1.92822	-4.25322	-4.22622	-1.95222	-2.64722	-3.21822	-
ermX	-1.26102	-1.85322	-3.36222	-3.13122	-1.90422	-1.86022	-3.30622	-1.87022

ermY	-3.98202	-3.50122	-	-	-	-3.71022	-4.16022	-	-3.41622
matA/mel	-1.57602	-2.66922	-2.97522	-3.29922	-	-2.75522	-2.74522	-3.83722	-
mdtA	-4.05402	-	-	-	-	-	-	-	-
mefA	-1.74402	-2.16022	-2.59422	-2.75622	-	-2.37022	-2.15722	-2.71122	-2.18022
oleC	-3.72102	-2.85022	-2.30622	-	-	-2.95922	-1.73522	-2.63422	-
vgaA-01	-4.89102	-3.69922	-	-	-	-	-	-	-
vgb-01	-5.60802	-	-3.46722	-4.19922	-	-2.76522	-3.07522	-3.23322	-4.63122
acrA-01	-2.50902	-	-	-	-	-	-	-	-
acrA-02	-2.42202	-	-	-	-	-	-	-	-
acrA-04	-5.63502	-3.79222	-3.37122	-	-	-3.56022	-	-3.69722	-4.07622
acrA-05	-	-3.58522	-	-3.55422	-	-2.82222	-3.11722	-3.16522	-3.58422
acrB-01	-2.13402	-	-	-	-	-	-	-4.24922	-
acrF	-2.12802	-	-	-	-	-	-	-4.35722	-
acrR-01	-5.33502	-	-	-	-	-	-	-	-
acrR-02	-2.26302	-	-	-	-	-	-	-4.03922	-
adeA	-5.46702	-	-	-	-	-3.57722	-	-	-
ceoA	-	-	-3.63222	-	-	-3.80922	-2.79922	-	-
cmr	-2.00202	-3.48322	-	-	-	-3.98622	-4.27672	-	-
emrD	-	-	-4.19322	-	-	-	-	-	-
floR	-0.55002	-1.86622	-3.41922	-3.31722	-	-1.38322	-1.84622	-2.17222	-1.89522
marR-01	-	-	-4.46022	-	-	-	-	-	-
mdtE/yhiU	-2.21802	-	-4.60422	-	-	-	-	-4.44122	-
mepA	-	-	-	-	-	-3.78522	-4.11022	-4.30022	-
mexA	-	-	-	-	-	-3.90822	-	-	-
mexE	-	-	-	-	-	-3.98322	-	-	-
mexF	-	-1.49722	-	-	-	-1.23322	-1.62822	-1.48022	-

dfrA1	-0.99102	-2.39522	-3.56622	-3.73422	-1.75322	-2.70222	-2.59322	-2.16522
dfrA12	-1.84002	-3.59722	-	-	-3.34422	-	-	-
folA	-5.66802	-	-	-	-	-	-	-
sul2	-0.68802	-1.19722	-2.92422	-2.21322	-1.20222	-1.51322	-1.15722	-0.95022
sulA/folP-01	-	-	-4.32822	-	-	-	-	-
sulA/folP-03	-	-	-4.09122	-	-	-	-	-
tet(32)	-2.59302	-	-3.89322	-4.07622	-3.65022	-3.66422	-4.28622	-4.58322
tet(36)-01	-1.99002	-	-	-	-3.85722	-	-	-
tet(36)-02	-2.48202	-	-	-	-3.76022	-	-	-
tetM-01	-0.61302	-2.42022	-2.65422	-2.84622	-2.06222	-2.45522	-3.28922	-2.92722
tetM-02	-1.19202	-3.37522	-3.32922	-3.48522	-2.98922	-3.50922	-4.31622	-3.85522
tetO-01	-2.11602	-	-3.47322	-3.78822	-3.38822	-3.15922	-3.63222	-4.55122
tetPB-01	-	-	-3.67422	-3.62922	-	-	-	-
tetPB-02	-	-	-	-3.95922	-	-	-	-4.65822
tetPB-03	-2.46402	-	-3.14922	-3.33222	-2.13022	-2.75722	-3.84022	-
tetPB-05	-	-	-3.79422	-3.36222	-	-	-	-
tetQ	-1.65102	-	-	-	-3.55522	-	-	-
tetS	-2.01102	-	-	-	-3.99422	-	-	-
tetT	-1.49202	-2.67922	-3.58422	-3.30222	-2.87422	-2.98822	-3.39022	-2.93022
tetA-02	-1.30602	-2.52322	-3.57822	-3.47022	-1.64722	-3.27422	-2.82422	-
tetB-01	-1.57302	-	-	-	-3.75622	-	-	-
tetB-02	-1.42002	-3.55222	-4.11522	-4.90122	-3.43022	-3.99722	-4.01422	-3.90222
tetC-01	-1.97202	-	-	-	-	-	-	-
tetC-02	-1.81902	-	-	-	-	-	-	-
tetD-01	-3.56802	-	-	-	-	-	-	-
tetD-02	-3.73602	-	-	-	-	-	-	-

tetE	-4.23402	-	-	-	-	-	-	-	-
tetG-01	-1.39002	-1.48722	-3.43122	-2.59122	-1.25822	-1.75022	-1.70122	-	-
tetG-02	-1.59102	-1.40422	-	-2.46222	-0.98222	-1.42822	-1.47922	-	-
tetH	-	-	-	-	-	-	-	-	-
tetJ	-3.77802	-	-	-	-	-	-	-	-
tetK	-4.21602	-	-	-	-	-	-	-	-
tetL-01	-	-	-4.56822	-	-3.85722	-	-4.18172	-	-
tetL-02	-1.08402	-1.15622	-3.22722	-3.38922	-1.36922	-1.78372	-2.54022	-1.72722	-
tetPA	-3.25002	-	-3.71022	-4.17822	-2.57622	-3.32122	-	-	-
tetR-02	-1.71702	-2.68322	-	-	-1.97322	-3.50522	-3.11922	-2.36622	-
tetR-03	-1.58502	-	-	-	-3.78622	-	-4.50722	-4.42722	-
tetV	-	-	-3.93222	-	-	-3.65422	-3.22522	-	-
tet(34)	-	-	-	-	-	-4.17022	-	-	-
tetX	-0.57402	-1.83622	-3.95022	-3.65322	-1.54222	-1.37022	-1.58522	-1.70022	-
IS613	-1.19802	-3.06222	-	-	-3.27122	-	-4.50322	-3.00822	-
tnpA-01	-2.69202	-3.76822	-	-	-	-3.75022	-	-	-
tnpA-02	-1.10502	-2.31622	-	-	-1.70472	-2.92822	-2.47822	-	-
tnpA-03	-1.88802	-3.70622	-	-	-4.12522	-	-	-3.72822	-
tnpA-04	-0.46002	0.01978	-2.42622	-1.82922	-0.26622	-0.72122	-1.12022	0.16778	-
tnpA-05	-0.32502	-2.51822	-3.90822	-3.34722	-1.70222	-2.71022	-2.44522	-2.32222	-
tnpA-07	-1.85202	-3.09022	-	-4.23522	-2.98422	-3.26222	-	-3.29522	-
Tp614	-2.31702	-	-	-	-4.34322	-	-4.02272	-4.69722	-
cIntI-1(class1)	-2.87802	-3.25672	-	-3.89322	-2.72022	-2.85722	-2.74322	-2.83872	-
intI-1(clinic)	-2.18802	-1.53422	-2.11422	-	-1.21922	-2.05822	-1.68622	-1.08522	-
vanA	-5.20602	-	-3.58122	-	-4.06122	-4.10272	-	-	-
vanB-01	-4.92402	-	-	-	-	-4.04872	-	-	-

